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NEWS 1		Web Page for STN Seminar Schedule - N. America
NEWS 2	JUN 06	EPFULL enhanced with 260,000 English abstracts
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NEWS 4	JUN 13	USPATFULL and USPAT2 updated with 11-character patent numbers for U.S. applications
NEWS 5	JUN 19	CAS REGISTRY includes selected substances from web-based collections
NEWS 6	JUN 25	CA/CAplus and USPAT databases updated with IPC reclassification data
NEWS 7	JUN 30	AEROSPACE enhanced with more than 1 million U.S. patent records
NEWS 8	JUN 30	EMBASE, EMBAL, and LEMBASE updated with additional options to display authors and affiliated organizations
NEWS 9	JUN 30	STN on the Web enhanced with new STN AnaVist Assistant and BLAST plug-in
NEWS 10	JUN 30	STN AnaVist enhanced with database content from EPFULL
NEWS 11	JUL 28	CA/CAplus patent coverage enhanced
NEWS 12	JUL 28	EPFULL enhanced with additional legal status information from the epoline Register
NEWS 13	JUL 28	IFICDB, IFIPAT, and IFIUDB reloaded with enhancements
NEWS 14	JUL 28	STN Viewer performance improved
NEWS 15	AUG 01	INPADOCDB and INPAFAMDB coverage enhanced
NEWS 16	AUG 13	CA/CAplus enhanced with printed Chemical Abstracts page images from 1967-1998
NEWS 17	AUG 15	CAOLD to be discontinued on December 31, 2008
NEWS 18	AUG 15	CAplus currency for Korean patents enhanced
NEWS 19	AUG 27	CAS definition of basic patents expanded to ensure comprehensive access to substance and sequence information
NEWS 20	SEP 18	Support for STN Express, Versions 6.01 and earlier, to be discontinued
NEWS 21	SEP 25	CA/CAplus current-awareness alert options enhanced to accommodate supplemental CAS indexing of exemplified prophetic substances
NEWS 22	SEP 26	WPIDS, WPINDEX, and WPIX coverage of Chinese and and Korean patents enhanced
NEWS 23	SEP 29	IFICLS enhanced with new super search field
NEWS 24	SEP 29	EMBASE and EMBAL enhanced with new search and display fields

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 NEWS 25  SEP 30  CAS patent coverage enhanced to include exemplified
                  prophetic substances identified in new Japanese-
                  language patents
 NEWS 26  OCT 07  EPFULL enhanced with full implementation of EPC2000
 NEWS 27  OCT 07  Multiple databases enhanced for more flexible patent
                  number searching
 NEWS 28  OCT 22  Current-awareness alert (SDI) setup and editing
                  enhanced
 NEWS 29  OCT 22  WPIDS, WPINDEX, and WPIX enhanced with Canadian PCT
                  Applications

 NEWS EXPRESS JUNE 27 08 CURRENT WINDOWS VERSION IS V8.3,
              AND CURRENT DISCOVER FILE IS DATED 23 JUNE 2008.

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FILE 'HOME' ENTERED AT 12:51:03 ON 23 OCT 2008

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COST IN U.S. DOLLARS                                SINCE FILE      TOTAL
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FILE 'REGISTRY' ENTERED AT 12:51:18 ON 23 OCT 2008
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DICTIONARY FILE UPDATES:  22 OCT 2008  HIGHEST RN 1064721-02-3

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=> s swefrt/sqsp
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FULL ESTIMATED COST 30.86 31.07

FILE 'HCAPLUS' ENTERED AT 12:51:47 ON 23 OCT 2008
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FILE COVERS 1907 - 23 Oct 2008 VOL 149 ISS 17
FILE LAST UPDATED: 22 Oct 2008 (20081022/ED)

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This file contains CAS Registry Numbers for easy and accurate substance identification.

=> l1
L2 10 L1

=> d l2 ibib abs hitstr 1-10

L2 ANSWER 1 OF 10 HCAPLUS COPYRIGHT 2008 ACS on STN
ACCESSION NUMBER: 2008:527000 HCAPLUS
DOCUMENT NUMBER: 149:2554
TITLE: Genomic and functional analysis of ICEPdaSpa1, a fish-pathogen-derived SXT-related integrating conjugative element that can mobilize a virulence plasmid
AUTHOR(S): Osorio, Carlos R.; Marrero, Joeli; Wozniak, Rachel A. F.; Lemos, Manuel L.; Burrus, Vincent; Waldor, Matthew K.
CORPORATE SOURCE: Microbiology and Genetics Programs, Tufts University

School of Medicine, Boston, MA, USA
SOURCE: Journal of Bacteriology (2008), 190(9), 3353-3361
CODEN: JOBAAY; ISSN: 0021-9193
PUBLISHER: American Society for Microbiology
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Integrating conjugative elements (ICEs) are self-transmissible mobile elements that transfer between bacteria via conjugation and integrate into the host chromosome. SXT and related ICEs became prevalent in Asian Vibrio cholerae populations in the 1990s and play an important role in the dissemination of antibiotic resistance genes in V. cholerae. Here, we carried out genomic and functional analyses of ICEPdaSpa1, an SXT-related ICE derived from a Spanish isolate of Photobacterium damselae subsp. piscicida, the causative agent of fish pasteurellosis. The .apprx.102-kb DNA sequence of ICEPdaSpa1 shows nearly 97% DNA sequence identity to SXT in genes that encode essential ICE functions, including integration and excision, conjugal transfer, and regulation. However, .apprx.25 kb of ICEPdaSpa1 DNA, including a tetracycline resistance locus, is not present in SXT. Most ICEPdaSpa1-specific DNA is inserted at loci where other SXT-related ICEs harbor element-specific DNA. ICEPdaSpa1 excises itself from the chromosome and is transmissible to other Photobacterium strains, as well as to Escherichia coli, in which it integrates into prfC. Interestingly, the P. damselae virulence plasmid pPHDP10 could be mobilized from E. coli in an ICEPdaSpa1-dependent fashion via the formation of a cointegrate between pPHDP10 and ICEPdaSpa1. PPHDP10-Cm integrated into ICEPdaSpa1 in a non-site-specific fashion independently of RecA. The ICEPdaSpa1::pPHDP10 cointegrates were stable, and markers from both elements became transmissible at frequencies similar to those observed for the transfer of ICEPdaSpa1 alone. Our findings reveal the plasticity of ICE genomes and demonstrate that ICEs can enable virulence gene transfer.

IT 1027485-86-4
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; sequences, genomic and functional anal. of ICEPdaSpa1, fish-pathogen-derived SXT-related integrating conjugative element that can mobilize virulence plasmid)
RN 1027485-86-4 HCAPLUS
CN Protein (Photobacterium damselae piscicida strain PC554.2 transposon ICEPdaSpa1 gene s088) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
REFERENCE COUNT: 36 THERE ARE 36 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 2 OF 10 HCAPLUS COPYRIGHT 2008 ACS on STN
ACCESSION NUMBER: 2006:54915 HCAPLUS
DOCUMENT NUMBER: 144:135452
TITLE: Combination therapy with apheresis for preventing or treating Alzheimer's disease, and kit therefor
INVENTOR(S): Mattner, Frank; Schmidt, Walter
PATENT ASSIGNEE(S): Austria
SOURCE: PCT Int. Appl., 25 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: German

FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2006005706	A2	20060119	WO 2005-EP53224	20050706
WO 2006005706	A3	20060720		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KM, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NG, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SM, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW				
RW: AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IS, IT, LT, LU, LV, MC, NL, PL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG, BW, GH, GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
AT 500483	A4	20060115	AT 2004-1185	20040713
AT 500483	B1	20060115		
AU 2005261687	A1	20060119	AU 2005-261687	20050706
CA 2577332	A1	20060119	CA 2005-2577332	20050706
EP 1765388	A2	20070328	EP 2005-767978	20050706
R: AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IS, IT, LI, LT, LU, LV, MC, NL, PL, PT, RO, SE, SI, SK, TR, AL, BA, HR, MK, YU				
CN 101022825	A	20070822	CN 2005-80023830	20050706
JP 2008506665	T	20080306	JP 2007-520813	20050706
US 20080051690	A1	20080228	US 2007-571970	20070111
KR 2007036158	A	20070402	KR 2007-702208	20070129
PRIORITY APPLN. INFO.:			AT 2004-1185 A	20040713
			WO 2005-EP53224 W	20050706

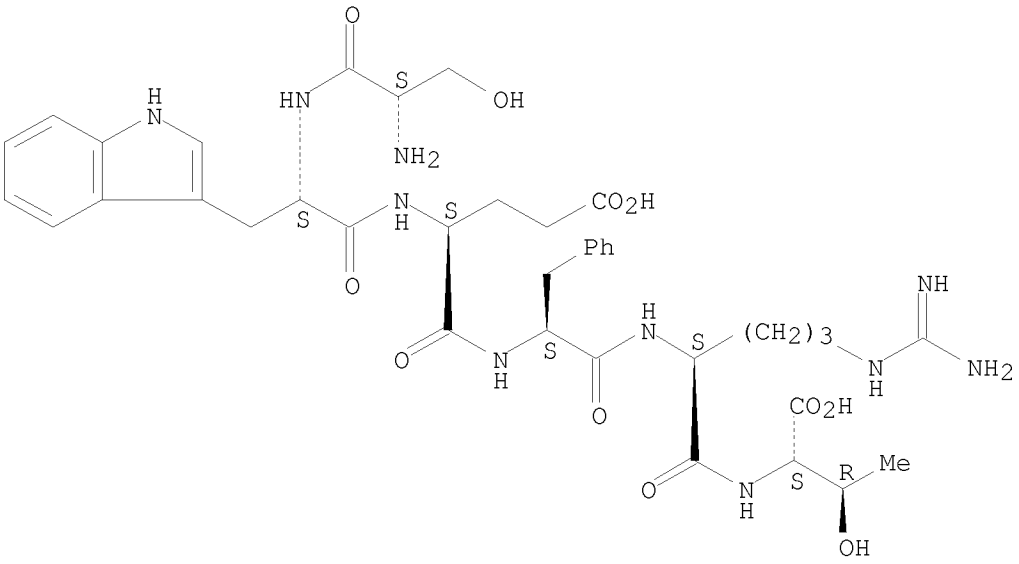
AB The invention relates to a method for preventing or treating Alzheimer's disease (AE). According to said method, a means for inducing a sequestration of amyloid β (Aβ) into a plasma is administered to a person, and the person is treated by means of an apheresis device comprising a fixed carrier that can come into contact with the blood or plasma flow and comprises a receptor binding an amyloid-β-precursor-protein (APP), the APP being removed from the blood of the person by means of the apheresis device. The invention also relates to a set for carrying out said method.

IT 727727-47-1
RL: THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(combination therapy with apheresis for preventing or treating Alzheimer's disease, and kit therefor)

RN 727727-47-1 HCAPLUS

CN L-Threonine, L-seryl-L-tryptophyl-L-α-glutamyl-L-phenylalanyl-L-arginyl- (9CI) (CA INDEX NAME)

Absolute stereochemistry.



L2 ANSWER 3 OF 10 HCAPLUS COPYRIGHT 2008 ACS on STN
ACCESSION NUMBER: 2006:51142 HCAPLUS
DOCUMENT NUMBER: 144:148852
TITLE: Vaccine for prevention and treatment of Alzheimer's disease
INVENTOR(S): Mattner, Frank; Schmidt, Walter
PATENT ASSIGNEE(S): Austria
SOURCE: PCT Int. Appl., 37 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2006005707	A2	20060119	WO 2005-EP53225	20050706
WO 2006005707	A3	20060817		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KM, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NG, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SM, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW				
RW: AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IS, IT, LT, LU, LV, MC, NL, PL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG, BW, GH, GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
AT 2004001184	A	20051115	AT 2004-1184	20040713
AT 413946	B	20060715		
AU 2005261688	A1	20060119	AU 2005-261688	20050706

CA 2573424	A1	20060119	CA 2005-2573424		20050706
EP 1765390	A2	20070328	EP 2005-769807		20050706
R: AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IS, IT, LI, LT, LU, LV, MC, NL, PL, PT, RO, SE, SI, SK, TR, AL, BA, HR, MK, YU					
CN 101043901	A	20070926	CN 2005-80030641		20050706
JP 2008506666	T	20080306	JP 2007-520814		20050706
KR 2007032033	A	20070320	KR 2007-702209		20070129
PRIORITY APPLN. INFO.:			AT 2004-1184	A	20040713
			WO 2005-EP53225	W	20050706

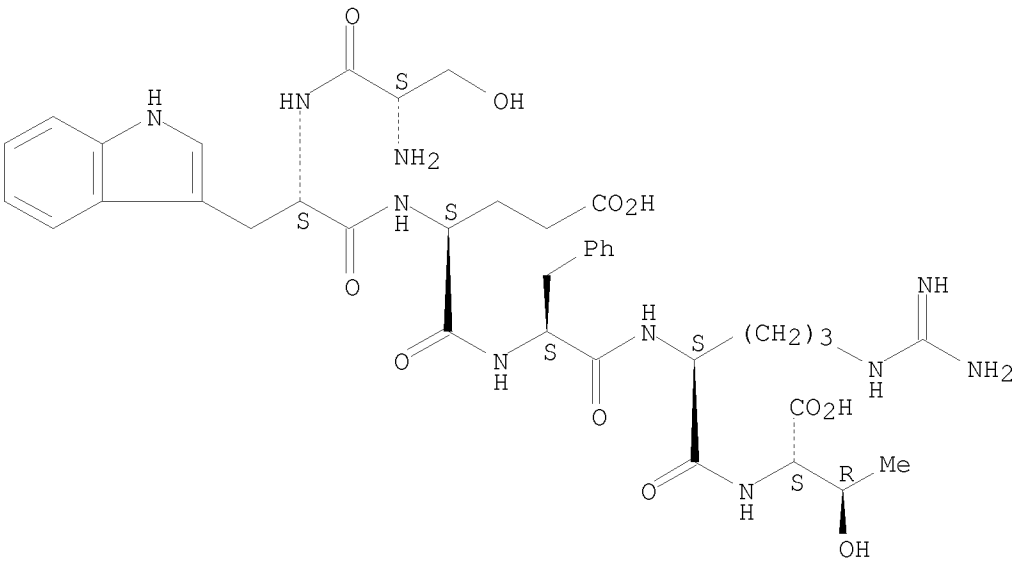
AB The author discloses the use of peptide mimotopes of the N-terminus of β-amyloid for vaccination against Alzheimer's disease. The mimotopes exhibit binding capacity for an antibody specific for the natural N-terminal sequence DAEFRH.

IT 727727-47-1
RL: PRP (Properties)
(unclaimed sequence; vaccine for prevention and treatment of Alzheimer's disease)

RN 727727-47-1 HCAPLUS

CN L-Threonine, L-seryl-L-tryptophyl-L-α-glutamyl-L-phenylalanyl-L-arginyl- (9CI) (CA INDEX NAME)

Absolute stereochemistry.



L2 ANSWER 4 OF 10 HCAPLUS COPYRIGHT 2008 ACS on STN

ACCESSION NUMBER: 2004:606544 HCAPLUS

DOCUMENT NUMBER: 141:152214

TITLE: Cell cycle progression genes and proteins of Drosophila melanogaster and their human homologs and their use for prevention, treatment and diagnosis of disease

INVENTOR(S): Glover, David; Bell, Graham; Frenz, Lisa; Midgley, Carol

PATENT ASSIGNEE(S): Cyclacel Limited, UK
SOURCE: PCT Int. Appl., 461 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2004063362	A2	20040729	WO 2003-GB5635	20031231
WO 2004063362	A3	20041202		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW				
RW: BW, GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
US 20050227301	A1	20051013	US 2003-745237	20031223
AU 2003290321	A1	20040810	AU 2003-290321	20031231
EP 1587916	A2	20051026	EP 2003-782680	20031231
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR, BG, CZ, EE, HU, SK				
JP 2006515754	T	20060608	JP 2005-512869	20031231
EP 1748065	A2	20070131	EP 2006-15664	20031231
R: AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LI, LU, MC, NL, PT, RO, SE, SI, SK, TR				

PRIORITY APPLN. INFO.:

US 2003-439123P	P	20030110
US 2003-468402P	P	20030506
EP 2003-782680	A3	20031231
WO 2003-GB5635	W	20031231

AB The invention describes human genes involved in cell cycle progression, including mitosis and meiosis. Candidate genes were identified by establishing their role in cell cell cycle progression through an RNAi-based knockdown approach in culture d Drosophila melanogaster cells followed by mitotic index evaluation (Cellomics Arrayscan). Human homologs are identified by performing a BLAST search and identifying the human protein with the best homol.; the role of the human genes are confirmed through RNAi in human cells followed by FACS anal. and microscopy. One hundred two Drosophila and human genes are identified and their transcript and encoded protein sequences provided. The invention also relates to the used of these "cell cycle progression" genes and proteins in the modulation of cell cycle progression in cells, and methods for identifying modulators of these genes or proteins and hence modulators of mitosis and meiosis.

IT 262973-73-9, GenBank AAF47396 727743-93-3
RL: BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(amino acid sequence; cell cycle progression genes and proteins of Drosophila melanogaster and their human homologs and their use for prevention, treatment and diagnosis of disease)

RN 262973-73-9 HCAPLUS

CN Protein (Drosophila melanogaster gene CG13893) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 727743-93-3 HCAPLUS
CN Protein (Drosophila melanogaster gene CG13893) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

L2 ANSWER 5 OF 10 HCAPLUS COPYRIGHT 2008 ACS on STN
ACCESSION NUMBER: 2004:606350 HCAPLUS
DOCUMENT NUMBER: 141:150981
TITLE: Methods for preventing and treating Alzheimer's disease (AD) using N-terminal Aβ42 peptide vaccines
INVENTOR(S): Mattner, Frank
PATENT ASSIGNEE(S): Austria
SOURCE: PCT Int. Appl., 29 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2004062556	A2	20040729	WO 2004-EP162	20040113
WO 2004062556	A3	20040916		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ				
AT 2003001464	A	20051115	AT 2003-1464	20030917
AT 413945	B	20060715		
AU 2004204349	A1	20040729	AU 2004-204349	20040113
CA 2513218	A1	20040729	CA 2004-2513218	20040113
EP 1583774	A2	20051012	EP 2004-701585	20040113
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR, BG, CZ, EE, HU, SK				
JP 2006515876	T	20060608	JP 2006-500553	20040113
EP 1679319	A1	20060712	EP 2005-107898	20040113
EP 1679319	B1	20071024		
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR, BG, CZ, EE, HU, SK				
CN 1826354	A	20060830	CN 2004-80002213	20040113
AT 376559	T	20071115	AT 2005-107898	20040113
ES 2296084	T3	20080416	ES 2005-107898	20040113
US 20060111301	A1	20060525	US 2005-540551	20051011

PRIORITY APPLN. INFO.:		
AT 2003-36	A	20030114
AT 2003-1464	A	20030917
EP 2004-701585	A3	20040113
WO 2004-EP162	W	20040113

OTHER SOURCE(S): MARPAT 141:150981
AB The invention relates to the use of a compound comprising the following amino acid sequence X1X2X3X4X5X6, wherein X1 is an amino acid, except of C, X2 is an amino acid, except of C, X3 is an amino acid, except of C, X4 is an amino acid, except of C, X5 is an amino acid, except of C, X6 is an

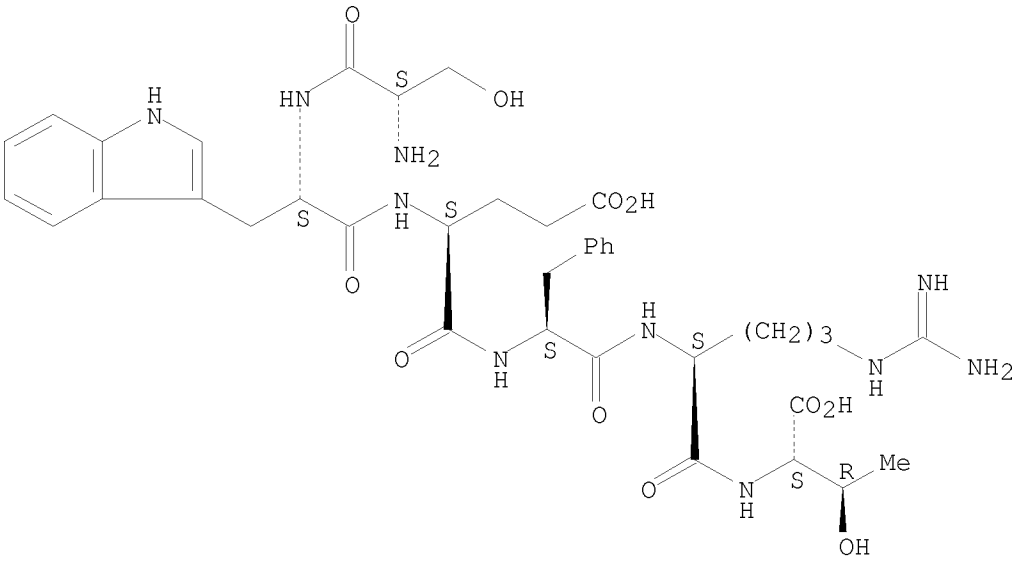
amino acid, except of C, and wherein X1X2X3X4X5X6 is not DAEFRH, said compound having a binding capacity to an antibody being specific for the natural N-terminal Aβ42 sequence DAEFRH, and 5-mers thereof having a binding capacity to said antibody being specific for the natural N-terminal Aβ42 sequence DAEFRH, for the preparation of a vaccine for Alzheimer's disease. Mimetopes of DAEFRH were identified by screening 6-mer peptide libraries for binding to an antibody to DAEFRH.

IT 727727-47-1
RL: BSU (Biological study, unclassified); PAC (Pharmacological activity); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(mimetope of natural N-terminal Aβ42 peptide; N-terminal Aβ42 peptide vaccines for preventing and treating Alzheimer's disease)

RN 727727-47-1 HCAPLUS

CN L-Threonine, L-seryl-L-tryptophyl-L-α-glutamyl-L-phenylalanyl-L-arginyl- (9CI) (CA INDEX NAME)

Absolute stereochemistry.



L2 ANSWER 6 OF 10 HCAPLUS COPYRIGHT 2008 ACS on STN

ACCESSION NUMBER: 2004:241801 HCAPLUS

DOCUMENT NUMBER: 140:248274

TITLE: EST and contig sequences of Drosophila melanogaster and their uses in microarrays, retrieval of full-length cDNAs and proteomic analysis, and for identification of pesticide targets

INVENTOR(S): Homburger, Sheila Akiko; Ebens, Allen James, Jr.; Erickson, Catherine Sue; Francis-Lang, Helen Louise; Margolis, Jonathan Scott; Reddy, Bindu Priya; Ruddy, David Andrew; Buchman, Andrew Roy

PATENT ASSIGNEE(S): Exelixis, Inc., USA

SOURCE: U.S., 262 pp.
CODEN: USXXAM

DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 19
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 6703491	B1	20040309	US 1999-270767	19990317
US 6703491	B1	20040309	US 1999-270767	19990317

PRIORITY APPLN. INFO.: US 1999-270767 A 19990317

AB The present invention relates to Drosophila genes and methods for their use. A library of 31,629 expressed sequence tags and contig sequences are provided from tissues of mixed-stage embryos (0-20 h), imaginal disks, and adult heads of Drosophila melanogaster. Drosophila ESTs and sequence contigs derived from ESTs are useful as tools for retrieval of full-length protein coding sequences, for proteomic anal., for use in microarrays and gene expression anal., and for identification of pesticide targets. Thus, the invention provides nucleotide sequences of Drosophila genes, amino acid sequences of the encoded proteins, and derivs. (e.g., fragments) and analogs thereof. Special emphasis is given to DNA sequences encoding G protein-coupled receptors and chitin synthetase. The invention further relates to fragments (and derivs. and analogs thereof) of proteins which comprise one or more domains of a Drosophila protein. Antibodies to Drosophila proteins, and derivs. and analogs thereof, are also provided. Also provided herein are vectors and host cells comprising such nucleic acids. Methods of production of a Drosophila protein (e.g., by recombination means), and derivs. and analogs thereof, are provided. Chimeric polypeptide mols. comprising polypeptides of the invention fused to heterologous polypeptide sequences are provided. Methods to identify the biol. function of a Drosophila gene are provided, including various methods for the functional modification (e.g., overexpression, underexpression, mutation, knock-out) of one gene, or of two or more genes simultaneously. [This abstract record is one of sixteen records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].

IT 669135-91-5
RL: AGR (Agricultural use); BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)
(amino acid sequence; EST and contig sequences of Drosophila melanogaster and their uses in microarrays, retrieval of full-length cDNAs and proteomic anal., and for identification of pesticide targets)

RN 669135-91-5 HCAPLUS
CN Protein (Drosophila melanogaster clone US6703491-SEQID-32985 fragment) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

L2 ANSWER 7 OF 10 HCAPLUS COPYRIGHT 2008 ACS on STN
ACCESSION NUMBER: 2003:130956 HCAPLUS
DOCUMENT NUMBER: 138:199733
TITLE: A Drosophila full-length cDNA resource
AUTHOR(S): Stapleton, Mark; Carlson, Joe; Brokstein, Peter; Yu, Charles; Champe, Mark; George, Reed; Guarin, Hannibal; Kronmiller, Brent; Pacleb, Joanne; Park, Soo; Wan, Ken; Rubin, Gerald M.; Celniker, Susan E.

CORPORATE SOURCE: Berkeley Drosophila Genome Project, Lawrence Berkeley National Lab., Berkeley, CA, USA
SOURCE: GenomeBiology (2002), 3(12), No pp. given
CODEN: GNBLFW; ISSN: 1465-6914
URL: http://genomebiology.com/content/pdf/gb-2002-3-12-research0080.pdf
PUBLISHER: BioMed Central Ltd.
DOCUMENT TYPE: Journal; (online computer file)
LANGUAGE: English

AB A collection of sequenced full-length cDNAs is an important resource both for functional genomics studies and for the determination of the intron-exon structure of genes. Providing this resource to the Drosophila melanogaster research community has been a long-term goal of the Berkeley Drosophila Genome Project. The Drosophila Gene Collection (DGC) has been previously described , a set of putative full-length cDNAs that was produced by generating and analyzing >250,000 expressed sequence tags (ESTs) derived from a variety of tissues and developmental stages. High-quality full-insert sequence were generated for 8921 clones in the DGC. The sequences of these clones were compared to the annotated Release 3 genomic sequence, and >5300 cDNAs identified that contain a complete and accurate protein-coding sequence. This corresponds to at least one splice form for 40% of the predicted D. melanogaster genes. Potential new cases of RNA editing were also identified. Thus, comparison of cDNA sequences to a high-quality annotated genomic sequence is an effective approach to identifying and eliminating defective clones from a cDNA collection. Clones were eliminated either because they carry single nucleotide discrepancies, which most probably result from reverse transcriptase errors, or because they are truncated and contain only part of the protein-coding sequence. [This abstract record is one of five records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].

IT 481877-77-4
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; full-length cDNA sequence resource for Drosophila melanogaster)

RN 481877-77-4 HCAPLUS

CN RE68566p (Drosophila melanogaster strain y; cn bw sp gene CG13893) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

L2 ANSWER 8 OF 10 HCAPLUS COPYRIGHT 2008 ACS on STN
ACCESSION NUMBER: 2002:678785 HCAPLUS
DOCUMENT NUMBER: 137:380859
TITLE: R391: a conjugative integrating mosaic comprised of phage, plasmid, and transposon elements
AUTHOR(S): Boltner, Dietmar; MacMahon, Claire; Pembroke, J. Tony; Strike, Peter; Osborn, A. Mark
CORPORATE SOURCE: Department of Biological Sciences, University of Essex, Colchester, CO4 3SQ, UK
SOURCE: Journal of Bacteriology (2002), 184(18), 5158-5169
CODEN: JOBAAY; ISSN: 0021-9193
PUBLISHER: American Society for Microbiology
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The conjugative, chromosomally integrating element R391 is the archetype of the IncJ class of mobile genetic elements. Originally found in a South African Providencia rettgeri strain, R391 carries antibiotic and mercury resistance traits, as well as genes involved in mutagenic DNA repair. While initially described as a plasmid, R391 has subsequently been shown to be integrated into the bacterial chromosome, employing a phage-like integration mechanism closely related to that of the SXT element from Vibrio cholerae O139. Anal. of the complete 89-kb nucleotide sequence of R391 has revealed a mosaic structure consisting of elements originating in bacteriophages and plasmids and of transposable elements. A total of 96 open reading frames were identified; of these, 30 could not be assigned a function. Sequence similarity suggests a relationship of large sections of R391 to sequences from Salmonella, in particular those corresponding to the putative conjugative transfer proteins, which are related to the IncHI1 plasmid R27. A composite transposon carrying the kanamycin resistance gene and a novel insertion element were identified. Challenging the previous assumption that IncJ elements are plasmids, no plasmid replicon was identified on R391, suggesting that they cannot replicate autonomously.

IT 476016-57-6
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; R391, a conjugative integrating mosaic comprised of phage, plasmid, and transposon elements)

RN 476016-57-6 HCAPLUS

CN Protein (Providencia rettgeri mobile element R391 255-amino acid) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

REFERENCE COUNT: 74 THERE ARE 74 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 9 OF 10 HCAPLUS COPYRIGHT 2008 ACS on STN

ACCESSION NUMBER: 2002:173239 HCAPLUS

DOCUMENT NUMBER: 136:396932

TITLE: Reagents and kits, such as nucleic acid arrays, for detecting the expression of over 10,000 Drosophila genes

INVENTOR(S): Venter, J. Craig; Adams, Mark; Li, Peter W. D.; Myers, Eugene W.

PATENT ASSIGNEE(S): PE Corporation (NY), USA

SOURCE: PCT Int. Appl., 21 pp.
CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 10

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001071042	A2	20010927	WO 2001-XG9231	20010323

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN,

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            YU, ZA, ZW
        RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY,
            DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF,
            BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG
    WO 2001071042        A2    20010927    WO 2001-US9231         20010323
    WO 2001071042        A3    20030313
        W:  AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN,
            CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM,
            HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS,
            LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO,
            RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN,
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            BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG
    US 20050208558       A1    20050922    US 2005-97143          20050404
PRIORITY APPLN. INFO.:                     US 2000-191637P     P  20000323
                                           US 2000-614150      A  20000711
                                           WO 2001-US9231      A  20010323
                                           US 1999-157832P     P  19991019
                                           US 1999-160191P     P  19991019
                                           US 1999-161932P     P  19991019
                                           US 1999-164769P     P  19991112
                                           US 1999-173383P     P  19991228
                                           US 2000-175693P     P  20000112
                                           US 2000-184831P     P  20000224
AB  The present invention is based on the sequencing and assembly of the
    Drosophila melanogaster genome.  The present invention provides the
    primary nucleotide sequence of a large portion of the Drosophila
    melanogaster genome in a series of genomic and predicted transcript
    sequences.  This information is provided in the form of genomic,
    transcript and protein sequence information and can be used to generate
    nucleic acid detection reagents and kits such as nucleic acid arrays.
    Primary sequences are provided as contiguous strings in a
    computer-readable format and recorded on media such as floppy disks, hard
    disks, magnetic tape, CD-ROM, RAM, ROM and hybrids of these categories.
    Genes/exons can be predicted,sequences can be edited and homol. searches
    of target motifs can be conducted.  [This abstract record is one of ten
    records for this document necessitated by the large number of index entries
    required to fully index the document and publication system constraints.].
IT  431288-23-2
    RL: ANT (Analyte); BSU (Biological study, unclassified); BUU (Biological
    use, unclassified); PRP (Properties); ANST (Analytical study); BIOL
    (Biological study); USES (Uses)
       (amino acid sequence; reagents and kits, such as nucleic acid arrays,
       for detecting the expression of over 10,000 Drosophila genes)
RN  431288-23-2  HCAPLUS
CN  Protein (Drosophila melanogaster clone WO0171042-SEQID-33039) (9CI)  (CA
    INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

L2  ANSWER 10 OF 10  HCAPLUS  COPYRIGHT 2008 ACS on STN
ACCESSION NUMBER:        2000:230405  HCAPLUS
DOCUMENT NUMBER:         132:304167
TITLE:                   The genome sequence of Drosophila melanogaster
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AUTHOR(S): Adams, Mark D.; Celniker, Susan E.; Holt, Robert A.; Evans, Cheryl A.; Gocayne, Jeannine D.; Amanatides, Peter G.; Scherer, Steven E.; Li, Peter W.; Hoskins, Roger A.; Galle, Richard F.; George, Reed A.; Lewis, Suzanna E.; Richards, Stephen; Ashburner, Michael; Henderson, Scott N.; Sutton, Granger G.; Wortman, Jennifer R.; Yandell, Mark D.; Zhang, Qing; Chen, Lin X.; Brandon, Rhonda C.; Rogers, Yu-Hui C.; Blazej, Robert G.; Champe, Mark; Pfeiffer, Barret D.; Wan, Kenneth H.; Doyle, Clare; Baxter, Evan G.; Helt, Gregg; Nelson, Catherine R.; Miklos, George L. Gabor; Abril, Josep F.; Agbayani, Anna; An, Hui-Jin; Andrews-Pfannkoch, Cynthia; Baldwin, Danita; Ballew, Richard M.; Basu, Anand; Baxendale, James; Bayraktaroglu, Leyla; Beasley, Ellen M.; Beeson, Karen Y.; Benos, P. V.; Berman, Benjamin P.; Bhandari, Deepali; Bolshakov, Slava; Borkova, Dana; Botchan, Michael R.; Bouck, John; Brokstein, Peter; Brottier, Phillipe; Burtis, Kenneth C.; Busam, Dana A.; Butler, Heather; Cadieu, Edouard; Center, Angela; Chandra, Ishwar; Cherry, J. Michael; Cawley, Simon; Dahlke, Carl; Davenport, Lionel B.; Davies, Peter; De Pablos, Beatriz; Delcher, Arthur; Deng, Zuoming; Mays, Anne Deslattes; Dew, Ian; Dietz, Suzanne M.; Dodson, Kristina; Doup, Lisa E.; Downes, Michael; Dugan-Rocha, Shannon; Dunkov, Boris C.; Dunn, Patrick; Durbin, Kenneth J.; Evangelista, Carlos C.; Ferraz, Concepcion; Ferriera, Steven; Fleischmann, Wolfgang; Foster, Carl; Gabrielian, Andrei E.; Garg, Neha S.; Gelbart, William M.; Glasser, Ken; Glodek, Anna; Gong, Fangcheng; Gorrell, J. Harley; Gu, Zhiping; Guan, Ping; Harris, Michael; Harris, Nomi L.; Harvey, Damon; Heiman, Thomas J.; Hernandez, Judith R.; Houck, Jarrett; Hostin, Damon; Houston, Kathryn A.; Howland, Timothy J.; Wei, Ming-Hui; Ibegwam, Chinyere; Jalali, Mena; Kalush, Francis; Karpen, Gary H.; Ke, Zhaoxi; Kennison, James A.; Ketchum, Karen A.; Kimmel, Bruce E.; Kodira, Chinnappa D.; Kraft, Cheryl; Kravitz, Saul; Kulp, David; Lai, Zhongwu; Lasko, Paul; Lei, Yiding; Levitsky, Alexander A.; Li, Jiayin; Li, Zhenya; Liang, Yong; Lin, Xiaoying; Liu, Xiangjun; Mattei, Bettina; McIntosh, Tina C.; McLeod, Michael P.; McPherson, Duncan; Merkulov, Gennady; Milshina, Natalia V.; Mobarry, Clark; Morris, Joe; Moshrefi, Ali; Mount, Stephen M.; Moy, Mee; Murphy, Brian; Murphy, Lee; Muzny, Donna M.; Nelson, David L.; Nelson, David R.; Nelson, Keith A.; Nixon, Katherine; Nusskern, Deborah R.; Pacleb, Joanne M.; Palazzolo, Michael; Pittman, Gjange S.; Pan, Sue; Pollard, John; Puri, Vinita; Reese, Martin G.; Reinert, Knut; Remington, Karin; Saunders, Robert D. C.; Scheeler, Frederick; Shen, Hua; Shue, Bixiang Christopher; Siden-Kiamos, Inga; Simpson, Michael; Skupski, Marian P.; Smith, Tom; Spier, Eugene; Spradling, Allan C.; Stapleton, Mark; Strong, Renee; Sun, Eric; Svirskas, Robert; Tector, Cyndee; Turner, Russell; Venter, Eli;

Wang, Aihui H.; Wang, Xin; Wang, Zhen-Yuan; Wassarman, David A.; Weinstock, George M.; Weissenbach, Jean; Williams, Sherita M.; Woodage, Trevor; Worley, Kim C.; Wu, David; Yang, Song; Yao, Q. Alison; Ye, Jane; Yeh, Ru-Fang; Zaveri, Jayshree S.; Zhan, Ming; Zhang, Guangren; Zhao, Qi; Zheng, Liansheng; Zheng, Xiangqun H.; Zhong, Fei N.; Zhong, Wenyan; Zhou, Xiaojun; Zhu, Shiaoping; Zhu, Xiaohong; Smith, Hamilton O.; Gibbs, Richard A.; Myers, Eugene W.; Rubin, Gerald M.; Venter, J. Craig

CORPORATE SOURCE: Celera Genomics, Rockville, MD, 20850, USA

SOURCE: Science (Washington, D. C.) (2000), 287(5461), 2185-2195
CODEN: SCIEAS; ISSN: 0036-8075

PUBLISHER: American Association for the Advancement of Science

DOCUMENT TYPE: Journal

LANGUAGE: English

AB The fly Drosophila melanogaster is one of the most intensively studied organisms in biol. and serves as a model system for the investigation of many developmental and cellular processes common to higher eukaryotes, including humans. The nucleotide sequence was determined of nearly all of the .apprx.120-megabase euchromatic portion of the Drosophila genome using a whole-genome shotgun sequencing strategy supported by extensive clone-based sequence and a high-quality bacterial artificial chromosome phys. map. Efforts are under way to close the remaining gaps; however, the sequence is of sufficient accuracy and contiguity to be declared substantially complete and to support an initial anal. of genome structure and preliminary gene annotation and interpretation. The genome encodes .apprx.13,600 genes, somewhat fewer than the smaller Caenorhabditis elegans genome, but with comparable functional diversity. Access to supporting information on each gene is available through FlyBase at http://flybase.bio.indiana.edu and through Celera at www.celera.com; the sequences are deposited in GenBank with Accession Nos. AE002566-AE003403. [This abstract record is one of 4 records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].

IT 262973-73-9
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; genome sequence of Drosophila melanogaster)

RN 262973-73-9 HCAPLUS

CN Protein (Drosophila melanogaster gene CG13893) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

REFERENCE COUNT: 89 THERE ARE 89 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

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=> S 669135-91-5/RN

L3 1 669135-91-5/RN

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L3 ANSWER 1 OF 1 REGISTRY COPYRIGHT 2008 ACS on STN
RN 669135-91-5 REGISTRY
CN Protein (Drosophila melanogaster clone US6703491-SEQID-32985 fragment)
(9CI) (CA INDEX NAME)
OTHER NAMES:
CN 985: PN: US6703491 SEQID: 32985 claimed protein
FS PROTEIN SEQUENCE
SQL 136

PATENT ANNOTATIONS (PNTE):
Sequence |Patent
Source |Reference
=========+==========
Not Given|US6703491

|claimed SEQID
|32985

SEQ 1 PEELYIDQSS QQSDRDFVEA QVPKGDKLKL HFKVNVEEQK ILSWEFRTFD
51 YDIKFGIYSV DDKTGEKRSE VPLGTVYSNE MDEIGYISTR PNTTYTVVFD
101 NSASYLRSKK LRYWVDLISE EEEGISELTT QMDNTQ
MF Unspecified
CI MAN
SR CA
LC STN Files: CA, CAPLUS, TOXCENTER
DT.CA CAplus document type: Patent
RL.P Roles from patents: BIOL (Biological study); PRP (Properties); USES (Uses)
1 REFERENCES IN FILE CA (1907 TO DATE)
1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

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